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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/464,099A

DATE: 07/19/2001

TIME: 15:37:51

Input Set : A:\MOBT175-2.ST25.txt

Output Set: N:\CRF3\07192001\I464099A.raw

PS

3 <110> APPLICANT: Barry, Gerard F.
 4 Kishore, Ganesh M.
 5 Padgett, Stephen R.
 6 Stallings, William C.
 8 <120> TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE
 SYNTHASES

ENTERED

10 <130> FILE REFERENCE: 11899.0175.CNUS01 MOBT:175-2
 12 <140> CURRENT APPLICATION NUMBER: 09/464,099A
 13 <141> CURRENT FILING DATE: 1999-12-16
 15 <150> PRIOR APPLICATION NUMBER: US 09/137,440
 16 <151> PRIOR FILING DATE: 1998-08-20
 18 <150> PRIOR APPLICATION NUMBER: US 08/833,485
 19 <151> PRIOR FILING DATE: 1997-04-07
 21 <150> PRIOR APPLICATION NUMBER: US 08/306,063
 22 <151> PRIOR FILING DATE: 1994-09-13
 24 <150> PRIOR APPLICATION NUMBER: US 07/749,611
 25 <151> PRIOR FILING DATE: 1991-08-28
 27 <150> PRIOR APPLICATION NUMBER: US 07/576,537
 28 <151> PRIOR FILING DATE: 1990-08-31
 30 <160> NUMBER OF SEQ ID NOS: 70
 32 <170> SOFTWARE: PatentIn version 3.0
 34 <210> SEQ ID NO: 1
 35 <211> LENGTH: 597
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Figwort mosaic virus
 39 <400> SEQUENCE: 1
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 42 actttattca aattggtatc gccaaaacca agaaggaact cccatcctca aagggtttgta 120
 44 aggaagaatt ctgagtcaca agcctcaaca aggtcagggt acagagtctc caaaccatta 180
 46 gccaaaagct acaggagatc aatgaagaat ctccaatcaa agtaaaactac tgttcagca 240
 48 catgcatcat ggtcagtaag ttccagaaaa agacatccac cgaagactta aagttagtgg 300
 50 gcatctttga aagtaattct gtcaacatcg agcagctggc ttgtggggac cagacaaaaa 360
 52 aggaatgggt cagaattggt aggcgcacct accaaaagca tctttgcctt tattgcaaag 420
 54 ataaagcaga ttcctctagt acaagtgggg aacaaaataa cgtggaaaag agctgtcctg 480
 56 acagcccaact cactaatgag tatgacgaac gcagtgcga ccacaaaaga attccctcta 540
 58 tataagaagg cattcattcc catttgaagg atcatcagat actaaccaat atttctc 597
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 62 <211> LENGTH: 1982
 63 <212> TYPE: DNA
 64 <213> ORGANISM: Agrobacterium sp.
 66 <220> FEATURE:
 67 <221> NAME/KEY: CDS
 68 <222> LOCATION: (62)..(1426)
 70 <400> SEQUENCE: 2
 71 aagcccgctg tctctccggc gctccgcccg gagagccgtg gatagattaa ggaagacgcc 60
 73 c atg tcg cac ggt gca agc agc cgg ccc gca acc gcc cgc aaa tcc tct 109
 74 Met Ser His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser
 75 1 5 10 15

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77	ggc	ctt	tcc	gga	acc	gtc	cgc	att	ccc	ggc	gac	aag	tcg	atc	tcc	cac	157
78	Gly	Leu	Ser	Gly	Thr	Val	Arg	Ile	Pro	Gly	Asp	Lys	Ser	Ile	Ser	His	
79				20				25					30				
81	cgg	tcc	ttc	atg	ttc	ggc	ggt	ctc	gcg	agc	ggt	gaa	acg	cgc	atc	acc	205
82	Arg	Ser	Phe	Met	Phe	Gly	Gly	Leu	Ala	Ser	Gly	Glu	Thr	Arg	Ile	Thr	
83			35					40					45				
85	ggc	ctt	ctg	gaa	ggc	gag	gac	gtc	atc	aat	acg	ggc	aag	gcc	atg	cag	253
86	Gly	Leu	Leu	Glu	Gly	Glu	Asp	Val	Ile	Asn	Thr	Gly	Lys	Ala	Met	Gln	
87		50					55					60					
89	gcc	atg	ggc	gcc	agg	atc	cgt	aag	gaa	ggc	gac	acc	tgg	atc	atc	gat	301
90	Ala	Met	Gly	Ala	Arg	Ile	Arg	Lys	Glu	Gly	Asp	Thr	Trp	Ile	Ile	Asp	
91	65					70				75			80				
93	ggc	gtc	ggc	aat	ggc	ggc	ctc	ctg	gcg	cct	gag	gcg	ccg	ctc	gat	ttc	349
94	Gly	Val	Gly	Asn	Gly	Gly	Leu	Leu	Ala	Pro	Glu	Ala	Pro	Leu	Asp	Phe	
95				85				90					95				
97	ggc	aat	gcc	gcc	acg	ggc	tgc	cgc	ctg	acc	atg	ggc	ctc	gtc	ggg	gtc	397
98	Gly	Asn	Ala	Ala	Thr	Gly	Cys	Arg	Leu	Thr	Met	Gly	Leu	Val	Gly	Val	
99			100					105					110				
101	tac	gat	ttc	gac	agc	acc	ttc	atc	ggc	gac	gcc	tcg	ctc	aca	aag	cgc	445
102	Tyr	Asp	Phe	Asp	Ser	Thr	Phe	Ile	Gly	Asp	Ala	Ser	Leu	Thr	Lys	Arg	
103			115					120					125				
105	ccg	atg	ggc	cgc	gtg	ttg	aac	ccg	ctg	cgc	gaa	atg	ggc	gtg	cag	gtg	493
106	Pro	Met	Gly	Arg	Val	Leu	Asn	Pro	Leu	Arg	Glu	Met	Gly	Val	Gln	Val	
107		130				135				140							
109	aaa	tcg	gaa	gac	ggt	gac	cgt	ctt	ccc	gtt	acc	ttg	cgc	ggg	ccg	aag	541
110	Lys	Ser	Glu	Asp	Gly	Asp	Arg	Leu	Pro	Val	Thr	Leu	Arg	Gly	Pro	Lys	
111	145					150				155			160				
113	acg	ccg	acg	ccg	atc	acc	tac	cgc	gtg	ccg	atg	gcc	tcc	gca	cag	gtg	589
114	Thr	Pro	Thr	Pro	Ile	Thr	Tyr	Arg	Val	Pro	Met	Ala	Ser	Ala	Gln	Val	
115				165				170					175				
117	aag	tcc	gcc	gtg	ctg	ctc	gcc	ggc	ctc	aac	acg	ccc	ggc	atc	acg	acg	637
118	Lys	Ser	Ala	Val	Leu	Leu	Ala	Gly	Leu	Asn	Thr	Pro	Gly	Ile	Thr	Thr	
119				180				185					190				
121	gtc	atc	gag	ccg	atc	atg	acg	cgc	gat	cat	acg	gaa	aag	atg	ctg	cag	685
122	Val	Ile	Glu	Pro	Ile	Met	Thr	Arg	Asp	His	Thr	Glu	Lys	Met	Leu	Gln	
123			195					200					205				
125	ggc	ttt	ggc	gcc	aac	ctt	acc	gtc	gag	acg	gat	gcg	gac	ggc	gtg	cgc	733
126	Gly	Phe	Gly	Ala	Asn	Leu	Thr	Val	Glu	Thr	Asp	Ala	Asp	Gly	Val	Arg	
127		210				215						220					
129	acc	atc	cgc	ctg	gaa	ggc	cgc	ggc	aag	ctc	acc	ggc	caa	gtc	atc	gac	781
130	Thr	Ile	Arg	Leu	Glu	Gly	Arg	Gly	Lys	Leu	Thr	Gly	Gln	Val	Ile	Asp	
131	225				230					235			240				
133	gtg	ccg	ggc	gac	ccg	tcc	tcg	acg	gcc	ttc	ccg	ctg	gtt	gcg	gcc	ctg	829
134	Val	Pro	Gly	Asp	Pro	Ser	Ser	Thr	Ala	Phe	Pro	Leu	Val	Ala	Ala	Leu	
135				245				250					255				
137	ctt	gtt	ccg	ggc	tcc	gac	gtc	acc	atc	ctc	aac	gtg	ctg	atg	aac	ccc	877
138	Leu	Val	Pro	Gly	Ser	Asp	Val	Thr	Ile	Leu	Asn	Val	Leu	Met	Asn	Pro	
139				260				265					270				
141	acc	cgc	acc	ggc	ctc	atc	ctg	acg	ctg	cag	gaa	atg	ggc	gcc	gac	atc	925

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142 Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
143      275      280      285
145 gaa gtc atc aac ccg cgc ctt gcc ggc ggc gaa gac gtg gcg gac ctg      973
146 Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
147      290      295      300
149 cgc gtt cgc tcc tcc acg ctg aag ggc gtc acg gtg ccg gaa gac cgc      1021
150 Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp Arg
151 305      310      315      320
153 gcg cct tcg atg atc gac gaa tat ccg att ctc gct gtc gcc gcc gcc      1069
154 Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala Ala
155      325      330      335
157 ttc gcg gaa ggg gcg acc gtg atg aac ggt ctg gaa gaa ctc cgc gtc      1117
158 Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg Val
159      340      345      350
161 aag gaa agc gac cgc ctc tcg gcc gtc gcc aat ggc ctc aag ctc aat      1165
162 Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu Asn
163      355      360      365
165 ggc gtg gat tgc gat gag ggc gag acg tcg ctc gtc gtg cgc ggc cgc      1213
166 Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly Arg
167      370      375      380
169 cct gac ggc aag ggg ctc ggc aac gcc tcg ggc gcc gcc gtc gcc acc      1261
170 Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala Thr
171 385      390      395      400
173 cat ctc gat cac cgc atc gcc atg agc ttc ctc gtc atg ggc ctc gtg      1309
174 His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val
175      405      410      415
177 tcg gaa aac cct gtc acg gtg gac gat gcc acg atg atc gcc acg agc      1357
178 Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser
179      420      425      430
181 ttc ccg gag ttc atg gac ctg atg gcc ggc ctg ggc gcg aag atc gaa      1405
182 Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile Glu
183      435      440      445
185 ctc tcc gat acg aag gct gcc tgatgacctt cacaatcgcc atcgatggtc      1456
186 Leu Ser Asp Thr Lys Ala Ala
187      450      455
189 ccgctgcggc cggcaagggg acgctctcgc gccgtatcgc ggaggtctat ggctttcatc      1516
191 atctcgatac gggcctgacc tatcgcgcca cggccaaagc gctgctcgat cgcggcctgt      1576
193 cgcttgatga cgaggcgggt gcggccgatg tcgcccgcaa tctcgatctt gccgggctcg      1636
195 accggtcggg gctgtcggcc catgccatcg gcgaggcggc ttcgaagatc gcggtcatgc      1696
197 cctcgggtcg gcgggcgctg gtcgaggcgc agcgagctt tgcggcgcgt gagccgggca      1756
199 cggtgctgga tggacgcgat atcggcacgg tggctctgcc ggatgcgccg gtgaagctct      1816
201 atgtcaccgc gtcaccggaa gtgcgcgcga aacgccgcta tgacgaaatc ctcggcaatg      1876
203 gcgggttggc cgattacggg acgatcctcg aggatatccg ccgccgcgac gagcgggaca      1936
205 tgggtcgggc ggacagtcct ttgaagcccg ccgacgatgc gcactt      1982
208 <210> SEQ ID NO: 3
209 <211> LENGTH: 455
210 <212> TYPE: PRT
211 <213> ORGANISM: Agrobacterium sp.
213 <400> SEQUENCE: 3

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215 Met Ser His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser
216 1 5 10 15
219 Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser His
220 20 25 30
223 Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
224 35 40 45
227 Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met Gln
228 50 55 60
231 Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile Asp
232 65 70 75 80
235 Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp Phe
236 85 90 95
239 Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly Val
240 100 105 110
243 Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys Arg
244 115 120 125
247 Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
248 130 135 140
251 Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro Lys
252 145 150 155 160
255 Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
256 165 170 175
259 Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr Thr
260 180 185 190
263 Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
264 195 200 205
267 Gly Phe Gly Ala Asn Leu Thr Val Glu Thr Asp Ala Asp Gly Val Arg
268 210 215 220
271 Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile Asp
272 225 230 235 240
275 Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
276 245 250 255
279 Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn Pro
280 260 265 270
283 Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
284 275 280 285
287 Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
288 290 295 300
291 Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp Arg
292 305 310 315 320
295 Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala Ala
296 325 330 335
299 Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg Val
300 340 345 350
303 Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu Asn
304 355 360 365
307 Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly Arg
308 370 375 380
311 Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala Thr

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312 385          390          395          400
315 His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val
316          405          410          415
319 Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser
320          420          425          430
323 Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile Glu
324          435          440          445
327 Leu Ser Asp Thr Lys Ala Ala
328          450          455
331 <210> SEQ ID NO: 4
332 <211> LENGTH: 1673
333 <212> TYPE: DNA
334 <213> ORGANISM: Agrobacterium sp.
336 <220> FEATURE:
337 <221> NAME/KEY: CDS
338 <222> LOCATION: (86)..(1432)
340 <400> SEQUENCE: 4
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343 gccaaaatgt gactgtgaaa aatcc atg tcc cat tct gca tcc ccg aaa cca 112
344          Met Ser His Ser Ala Ser Pro Lys Pro
345          1          5
347 gca acc gcc cgc cgc tcg gag gca ctc acg ggc gaa atc cgc att ccg 160
348 Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg Ile Pro
349 10          15          20          25
351 ggc gac aag tcc atc tcg cat cgc tcc ttc atg ttt ggc ggt ctc gca 208
352 Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu Ala
353          30          35          40
355 tcg ggc gaa acc cgc atc acc ggc ctt ctg gaa ggc gag gac gtc atc 256
356 Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp Val Ile
357          45          50          55
359 aat aca ggc cgc gcc atg cag gcc atg ggc gcg aaa atc cgt aaa gag 304
360 Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg Lys Glu
361          60          65          70
363 ggc gat gtc tgg atc atc aac ggc gtc ggc aat ggc tgc ctg ttg cag 352
364 Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu Leu Gln
365          75          80          85
367 ccc gaa gct gcg ctc gat ttc ggc aat gcc gga acc ggc gcg cgc ctc 400
368 Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala Arg Leu
369 90          95          100          105
371 acc atg ggc ctt gtc ggc acc tat gac atg aag acc tcc ttt atc ggc 448
372 Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe Ile Gly
373          110          115          120
375 gac gcc tcg ctg tcg aag cgc ccg atg ggc cgc gtg ctg aac ccg ttg 496
376 Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn Pro Leu
377          125          130          135
379 cgc gaa atg ggc gtt cag gtg gaa gca gcc gat ggc gac cgc atg ccg 544
380 Arg Glu Met Gly Val Gln Val Glu Ala Ala Asp Gly Asp Arg Met Pro
381          140          145          150
383 ctg acg ctg atc ggc ccg aag acg gcc aat ccg atc acc tat cgc gtg 592

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:1278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1355 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1443 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:1550 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:1569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:2605 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54